IFWO

RAW SEQUENCE LISTING   DATE: 08/02/2004
PATENT APPLICATION: US/10/724,301   TIME: 15:07:13

Input Set : A:\1-1411 SEQUENCE LISTING.txt
Output Set: N:\CRF4\08022004\J724301.raw

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 3 <110> APPLICANT: Enenkel, Barbara
 4        Fieder, Juergen
 5        Otto, Ralf
 6        Sautter, Kerstin
 7        Bergemann, Klaus
 9 <120> TITLE OF INVENTION: Neomycin-Phosphotransferase Genes and Methods
10        for the Selection of Recombinant Cells Producing
11        High Levels of a Desired Gene Product
13 <130> FILE REFERENCE: 1/1411
15 <140> CURRENT APPLICATION NUMBER: US/10/724,301
16 <141> CURRENT FILING DATE: 2003-11-26
18 <150> PRIOR APPLICATION NUMBER: US 60/431,535
19 <151> PRIOR FILING DATE: 2002-12-06
21 <150> PRIOR APPLICATION NUMBER: US 60/487,902
22 <151> PRIOR FILING DATE: 2003-07-17
24 <150> PRIOR APPLICATION NUMBER: DE 102 56 081
25 <151> PRIOR FILING DATE: 2002-11-29
27 <150> PRIOR APPLICATION NUMBER: DE 103 30 686
28 <151> PRIOR FILING DATE: 2003-07-08
30 <160> NUMBER OF SEQ ID NOS: 55
32 <170> SOFTWARE: PatentIn Ver. 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 795
36 <212> TYPE: DNA
37 <213> ORGANISM: Escherichia coli
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41 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 120
42 gcgcagggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
43 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
44 ctcgacgttg tcactgaagc gggaagggac tggctgctat tgggcgaagt gccggggcag 300
45 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
46 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
47 atcgagcgag cacgtactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa 480
48 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgac 540
49 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
50 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
51 atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
52 ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
53 gacgagttct tctga                                                795
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 264
58 <212> TYPE: PRT
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63   1               5                  10                  15
65  Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
66              20                  25                  30
68  Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
69          35                  40                  45
71  Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
72      50                  55                  60
74  Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
75  65                  70                  75                  80
77  Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
78              85                  90                  95
80  Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
81              100                 105                 110
83  Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
84          115                 120                 125
86  Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
87      130                 135                 140
89  Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
90  145                 150                 155                 160
92  Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
93              165                 170                 175
95  Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
96              180                 185                 190
98  Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
99          195                 200                 205
101 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
102     210                 215                 220
104 Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
105 225                 230                 235                 240
107 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
108                 245                 250                 255
110 Tyr Arg Leu Leu Asp Glu Phe Phe
111                 260
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 795
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: Neomycin mutant E182G
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124 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 120
125 gcgcagggg gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
126 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
127 ctcgacgttg tcactgaagc gggaagggac tggctgctat tgggcgaagt gccggggcag 300
128 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
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129 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
130 atcgagcgag cacgtactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa 480
131 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgac 540
132 ggcggggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
133 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
134 atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
135 ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
136 gacgagttct tctga                                                   795
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139 <210> SEQ ID NO: 4
140 <211> LENGTH: 264
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Neomycin mutant E182G
147 <400> SEQUENCE: 4

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149  1               5                  10                  15
151 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
152             20                  25                  30
154 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
155         35                  40                  45
157 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
158     50                  55                  60
160 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
161 65                  70                  75                  80
163 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
164             85                  90                  95
166 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
167         100                 105                 110
169 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
170         115                 120                 125
172 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
173     130                 135                 140
175 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
176 145                 150                 155                 160
178 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
179             165                 170                 175
181 Ser Met Pro Asp Gly Gly Asp Leu Val Val Thr His Gly Asp Ala Cys
182             180                 185                 190
184 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
185         195                 200                 205
187 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
188     210                 215                 220
190 Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
191 225                 230                 235                 240
193 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
194             245                 250                 255
196 Tyr Arg Leu Leu Asp Glu Phe Phe
197             260
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201 <211> LENGTH: 795
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Neomycin mutant W91A
208 <400> SEQUENCE: 5
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210 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 120
211 gcgcagggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
212 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
213 ctcgacgttg tcactgaagc gggaagggac gcgctgctat gggcgaagt gccgggggcag 300
214 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
215 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
216 atcgagcgag cacgtactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa 480
217 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgac 540
218 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
219 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
220 atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
221 ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
222 gacgagttct tctga                                                   795
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226 <211> LENGTH: 264
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Neomycin mutant W91A
233 <400> SEQUENCE: 6
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238                20                  25                  30
240 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
241             35                  40                  45
243 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
244          50                  55                  60
246 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
247  65                  70                  75                  80
249 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Ala Leu Leu Leu Gly Glu
250                85                  90                  95
252 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
253             100                 105                 110
255 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
256             115                 120                 125
258 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
259          130                 135                 140
261 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
262 145                 150                 155                 160
264 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
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265                  165                170                175
267 Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
268             180                185                190
270 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
271         195                200                205
273 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
274     210                215                220
276 Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
277 225             230                235                240
279 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
280             245                250                255
282 Tyr Arg Leu Leu Asp Glu Phe Phe
283         260
286 <210> SEQ ID NO: 7
287 <211> LENGTH: 795
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Neomycin mutant V198G
294 <400> SEQUENCE: 7
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296 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 120
297 gcgcagggg c gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
298 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
299 ctcgacgttg tcactgaagc gggaagggac tggctgctat tgggcgaagt gccggggcag 300
300 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
301 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
302 atcgagcgag cacgtactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa 480
303 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgac 540
304 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggggggaaaat 600
305 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
306 atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
307 ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
308 gacgagttct tctga                                                    795
311 <210> SEQ ID NO: 8
312 <211> LENGTH: 264
313 <212> TYPE: PRT
314 <213> ORGANISM: Artificial sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Neomycin mutant V198G
319 <400> SEQUENCE: 8
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324             20                25                30
326 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
327         35                40                45
329 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
330     50                55                60
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VERIFICATION SUMMARY   DATE: 08/02/2004
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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number